

SEQUENCE LISTING

SEQ ID NO:1

X-Sun-Data-Type: text

5 X-Sun-Data-Description: text

X-Sun-Data-Name: text

X-Sun-Charset: us-ascii

X-Sun-Content-Lines: 11

menin.cDNA 1.28, 2772 bases

10 1 GGTGTCCGGA GCCGCGGACC TAGAGATCCC AGAAGCCACA GCGCAGCGGC
51 CCGGCCCCGCC ACTATTTCCA GGCTCTGCGG GCCAGGGGCC GCCGCCCACC
101 GCCCGCCGCC ATGGGGCTGA AGGCCGCCCA GAAGACGCTG TTCCCGCTGC
151 GCTCCATCGA CGACGTGGTG CGCCTGTTTG CTGCCGAGCT GGGCCGAGAG
201 GAGCCGGACC TGGTGCTCCT TTCCTTGGTG CTGGGCTTCG TGGAGCATTT
15 251 TCTGGCTGTC AACC GCGTCA TCCCTACCAA CGTTCCCGAG CTCACCTTCC
301 AGCCCAGCCC CGCCCCGAC CCGCCTGGCG GCCTCACCTA CTTTCCCGTG
351 GCCGACCTGT CTATCATCGC CGCCCTCTAT GCCCGCTTCA CCGCCCAGAT
401 CCGAGGCGCC GTCGACCTGT CCCTCTATCC TCGAGAAGGG GGTGTCTCCA
451 GCCGTGAGCT GGTGAAGAAG GTCTCCGATG TCATATGGAA CAGCCTCAGC
20 501 CGCTCCTACT TCAAGGATCG GGCCCACATC CAGTCCCTCT TCAGCTTCAT
551 CACAGGCACC AAATTGGACA GCTCCGGTGT GGCCTTTGCT GTGGTTGGGG
601 CCTGCCAGGC CCTGGGTCTC CGGGATGTCC ACCTCGCCCT GTCTGAGGAT
651 CATGCCTGGG TAGTGTTTGG GCCCAATGGG GAGCAGACAG CTGAGGTCAC
701 CTGGCACGGC AAGGGCAACG AGGACCGCAG GGGCCAGACA GTCAATGCCC
25 751 GTGTGGCTGA GCGGAGCTGG CTGTACCTGA AAGGATCATA CATGCGCTGT
801 GACCGCAAGA TGGAGGTGGC GTTCATGGTG TGTGCCATCA ACCCTTCCAT
851 TGACCTGCAC ACCGACTCGC TGGAGCTTCT GCAGCTGCAG CAGAAGCTGC
901 TCTGGCTGCT CTATGACCTG GGACATCTGG AAAGGTACCC CATGGCCTTA
951 GGGAACCTGG CAGATCTAGA GGAGCTGGAG CCCACCCCTG GCCGGCCAGA
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1101 AACC GCAATG TGCGGGAAGC CCTGCAGGCC TGGGCGGACA CGGCCACTGT
1151 CATCCAGGAC TACA ACTACT GCCGGGAAGA CGAGGAGATC TACAAGGAGT
1201 TCTTTGAAGT AGCCAATGAT GTCATCCCCA ACCTGCTGAA GGAGGCAGCC
35 1251 AGCTTGCTGG AGGCGGGCGA GGAGCGGCCG GGGGAGCAAA GCCAGGGCAC
1301 CCAGAGCCAA GGTTCCGCCC TCCAGGACCC TGAGTGCTTC GCCCACCTGC
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1401 GTGCTGCACG TGGGCTGGGC CACCTTTCTT GTGCAGTCCC TAGGCCGTTT
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1501 CGGCCGAGGC CGAGGAGCCG TGGGGCGAGG AAGCCCGGGA AGGCCGGCGG
1551 CGGGGCCCCAC GGCGGGAGTC CAAGCCAGAG GAGCCCCCGC CGCCCAAGAA
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2201 TAATTACCAG TCTTTAAAGG CCCAGCCCCT AGAAACCCAA GTCCTCCTC
2251 GGAACCGCTC ACCTAGAGCC AGACCAACGT TACTCAGGGC TCCTCCAGC
2301 TTGTAGGAGC TGAGGTTTCA CCCTTAACCC AAGGGAGCAC AGGTCCCACC
2351 TCCAGCCCGG GGAGCCTAGG ACCACTCAGC CCCTAGGAGT ATATTTCCGC
2401 ACTTCAGAAT TCCATATCTT GCGAATCCAA GTCCTCGCC CCAAATAACT
2451 TCAGTCCTGC TTCCAGAATT TGGAATCCT AGTTTCCTCT CCTTCGTATC
2501 CCGAGTCTGG GACACAAAAC TCCGCCCCCA GCCTATGAGC ATCCTGAGCC
2551 CCGCCCTCTT CCTGACGAAA CTGGCCCCCG ATCAGAGCAG GACCTCCCTT
2601 CCGACCCTCT GGGAACCTCC CAGAGGTCCA GCCCATCTCG GAGCATCCCG
2651 GAGGAAATCT GCAGAGGGGT TAGGAGTGGG TGACAAGAGC CTGATCTCTT
2701 CCTGTTTTGT ACATAGATTT ATTTTTCAGT TCCAAGAAAG ATGAATACAT
2751 TTTGTTAAAA AAAAAAAAAA AA

SEQ ID NO:2

Mu.prot sequence 610 amino acids

1 MGLKAAQKTL FPLRSIDDVV RLFAAELGRE EPDLVLLSLV LGFVEHFLAV
51 NRVIPTNVPE LTFQPSAPD PPGGLTYFPV ADLSIIAALY ARFTAQIRGA
101 VDLSLYPREG GVSSREL VKK VSDVTWNSLS RSYFKDRAHI QSLFSFITGT
151 KLDSSGVAFA VVGACQALGL RDVHLALSED HAWVVFPGNG EQTA EVTWHG
201 KGNEDRRGQT VNAGVAERSW LYLKGSYMRC DRKMEVAFMV CAINPSIDLH
251 TDSLELLQLQ QKLLWLLYDL GHLEYPMAL GNLADLEELE PTPGRPDPLT
301 LYHKGIASAK TYRDEHIYP YMYLAGYHCR NRVREALQA WADTATVIQD

351 YNYCREDEEI YKEFFEVDND VIPNLLKEAA SLLEAGEERP GEQSQGTQSQ
401 GSALQDPECF AHLLRFYDGI CKWEEGSPTP VLHVGWATFL VQSLGRFEGQ
451 VRQKVRIYSR EAEAAEAEEP WGEEAREGRR RGPRRESKPE EPPPPKKPAL
501 DKGLGTGQGA VSGPPRKPPG TVAGTARGPE GGSTAQVPAP AASPPPEGPV
551 LTFQSEKMKG MKELLVATKI NSSAIKLQLT AQSQVQMKKQ KVESTPSDYTL
601 SFLKRQRKGL

SEQ ID NO:3

The genomic sequence for the *MEN1* gene

mu_genomic.fa 9180 bp

1 CTGGTCTTGA ACTCCTGGCC TCAAGCAATC CTCCTGCTTC AGCTTCCCAA
51 AGTGTGTGTA TTACAGGCAT GAGCCTGGCA TGAAGTTGAC ACTATTGAGA
101 TATACTGGTC AGGTATTTTG TGAATGTCC CTCAACTCTG TTTTGCCAGA
151 TGTCTTCTCA TGATTAGAGG AGAGTTATAA ATTTTGAGGA AAATCCAGAG
201 AGGTGAAGAG GTGAAGTAGG GCAGAAATTT AATCTGTTTT ATTTACTGCT
251 ATATACCGAG TGTCTGGAAC TTGGCCCATG GTAAGTACCA AAAATCTGTT
301 TTTTTTGAAT GAATAAGCAA ATAAATGAGT GACCGTGGAA ATTTAGTATT
351 ATTTCAAAGT TTCAAAGCGT TGTTGATACA GGCCAGGCAC AGTGGCTCAC
401 ACCTGTAATC CCAGCACTTT TGGAGGCCGA GGTAGGAGGA TCACTTGAGG
451 TCAGGAGTTC GAGACCAGCC TGACCAACAT GGTGACACCC CTGTCTCTAC
501 TAAGTAAAAT AAAAAAATTA GCCAAGTGTG GTGGCAGGCA CCTGTAATCC
551 CGGCTACTTG GGAAGCTGAG GCAGAAGAAT CACTTGAACC TGGGAGGCAG
601 AGGTTGCAGT GAGCCGAGAT CACCCCACTG CACTCCAGCC TGAGTGACAG
651 AGCGAGACTC TGTCTCAAAA CAAATAAACA AATAACTACT CTTTGGCCGG
701 GTAAGGTGGT TCACGCCTGT AATTTTAGCA CTTTGGGAGG CTGAGGCGGG
751 CAGATCACTT GAGGTTAGGG GTTCGAGACC AGTCTGGCCA ACATGGTGAA
801 ACCCCATCTC TACTTAAAT AAAAAAGTT TTCTGGGTGT GGTGGCGGAC
851 GCCTATAATC CCAGCTACTT GGGACTTTTT TTTAAGACGG AATCTCACTC
901 TGTGCCCCAG GCTGGAGTGC AGTGGCAAGA TTCTGGCTCA CTGAAGCCTC
951 CGCCTCCCAG GTTCAAGGGG ATTCCCCGCG CCTCAGCCTC CCAAGTAGCT
1001 GGAATCCCT GTCTCTGCAA AAAAAAAAAA AAAAAAAAAAC AAAAAATATA
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1151 GCACGCCTGT GATCACAGCT ACTCGGGAGG CTGAGGCACG AGAATCGCTT
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2251 GGCTTGCTT GCAGGCCGCC GCCCACC GCCCGCCATG GGGCTGAAGG
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